

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/789,526A
Source: JFWL6
Date Processed by STIC: 9/19/06

ENTERED



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/789,526A

DATE: 09/19/2006

TIME: 13:18:04

Input Set : A:\PTO.SS.txt

Output Set: N:\CRF4\09192006\J789526A.raw

(pg. 6-7)

3 <110> APPLICANT: George Tachas
 4 Kenneth W. Dobie
 5 Ravi Jain
 6 Christopher Ian Belyea
 7 Mark Andrew Heffernan
 9 <120> TITLE OF INVENTION: MODULATION OF GROWTH HORMONE RECEPTOR EXPRESSION AND
 10 INSULIN LIKE GROWTH FACTOR EXPRESSION
 12 <130> FILE REFERENCE: BIOL0002US
 14 <140> CURRENT APPLICATION NUMBER: 10/789,526A
 15 <141> CURRENT FILING DATE: 2004-02-26
 17 <150> PRIOR APPLICATION NUMBER: 60/451,455
 18 <151> PRIOR FILING DATE: 2003-02-28
 20 <160> NUMBER OF SEQ ID NOS: 272
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 20
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Artificial Sequence
 28 <220> FEATURE:
 30 <223> OTHER INFORMATION: Antisense Oligonucleotide
 32 <400> SEQUENCE: 1
 33 tccgtcatcg ctcctcaggg 20
 36 <210> SEQ ID NO: 2
 37 <211> LENGTH: 20
 38 <212> TYPE: DNA
 39 <213> ORGANISM: Artificial Sequence
 41 <220> FEATURE:
 43 <223> OTHER INFORMATION: Antisense Oligonucleotide
 45 <400> SEQUENCE: 2
 46 gtgcgcgcga gccccaaatc 20
 49 <210> SEQ ID NO: 3
 50 <211> LENGTH: 20
 51 <212> TYPE: DNA
 52 <213> ORGANISM: Artificial Sequence
 54 <220> FEATURE:
 56 <223> OTHER INFORMATION: Antisense Oligonucleotide
 58 <400> SEQUENCE: 3
 59 atgcattctg cccccaagga 20
 62 <210> SEQ ID NO: 4
 63 <211> LENGTH: 4414
 64 <212> TYPE: DNA
 65 <213> ORGANISM: H. sapiens
 67 <220> FEATURE:
 69 <220> FEATURE:

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71 <222> LOCATION: (44)...(1960)
73 <400> SEQUENCE: 4
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75 Met Asp Leu Trp
76 1
78 cag ctg ctg ttg acc ttg gca ctg gca gga tca agt gat gct ttt tct 103
79 Gln Leu Leu Leu Thr Leu Ala Leu Ala Gly Ser Ser Asp Ala Phe Ser
80 5 10 15 20
82 gga agt gag gcc aca gca gct atc ctt agc aga gca ccc tgg agt ctg 151
83 Gly Ser Glu Ala Thr Ala Ala Ile Leu Ser Arg Ala Pro Trp Ser Leu
84 25 30 35
86 caa agt gtt aat cca ggc cta aag aca aat tct tct aag gag cct aaa 199
87 Gln Ser Val Asn Pro Gly Leu Lys Thr Asn Ser Ser Lys Glu Pro Lys
88 40 45 50
90 ttc acc aag tgc cgt tca cct gag cga gag act ttt tca tgc cac tgg 247
91 Phe Thr Lys Cys Arg Ser Pro Glu Arg Glu Thr Phe Ser Cys His Trp
92 55 60 65
94 aca gat gag gtt cat cat ggt aca aag aac cta gga ccc ata cag ctg 295
95 Thr Asp Glu Val His His Gly Thr Lys Asn Leu Gly Pro Ile Gln Leu
96 70 75 80
98 ttc tat acc aga agg aac act caa gaa tgg act caa gaa tgg aaa gaa 343
99 Phe Tyr Thr Arg Arg Asn Thr Gln Glu Trp Thr Gln Glu Trp Lys Glu
100 85 90 95 100
102 tgc cct gat tat gtt tct gct ggg gaa aac agc tgt tac ttt aat tca 391
103 Cys Pro Asp Tyr Val Ser Ala Gly Glu Asn Ser Cys Tyr Phe Asn Ser
104 105 110 115
106 tcg ttt acc tcc atc tgg ata cct tat tgt atc aag cta act agc aat 439
107 Ser Phe Thr Ser Ile Trp Ile Pro Tyr Cys Ile Lys Leu Thr Ser Asn
108 120 125 130
110 ggt ggt aca gtg gat gaa aag tgt ttc tct gtt gat gaa ata gtg caa 487
111 Gly Gly Thr Val Asp Glu Lys Cys Phe Ser Val Asp Glu Ile Val Gln
112 135 140 145
114 cca gat cca ccc att gcc ctc aac tgg act tta ctg aac gtc agt tta 535
115 Pro Asp Pro Pro Ile Ala Leu Asn Trp Thr Leu Leu Asn Val Ser Leu
116 150 155 160
118 act ggg att cat gca gat atc caa gtg aga tgg gaa gca cca cgc aat 583
119 Thr Gly Ile His Ala Asp Ile Gln Val Arg Trp Glu Ala Pro Arg Asn
120 165 170 175 180
122 gca gat att cag aaa gga tgg atg gtt ctg gag tat gaa ctt caa tac 631
123 Ala Asp Ile Gln Lys Gly Trp Met Val Leu Glu Tyr Glu Leu Gln Tyr
124 185 190 195
126 aaa gaa gta aat gaa act aaa tgg aaa atg atg gac cct ata ttg aca 679
127 Lys Glu Val Asn Glu Thr Lys Trp Lys Met Met Asp Pro Ile Leu Thr
128 200 205 210
130 aca tca gtt cca gtg tac tca ttg aaa gtg gat aag gaa tat gaa gtg 727
131 Thr Ser Val Pro Val Tyr Ser Leu Lys Val Asp Lys Glu Tyr Glu Val
132 215 220 225
134 cgt gtg aga tcc aaa caa cga aac tct gga aat tat ggc gag ttc agt 775

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135	Arg	Val	Arg	Ser	Lys	Gln	Arg	Asn	Ser	Gly	Asn	Tyr	Gly	Glu	Phe	Ser		
136	230					235				240								
138	gag	gtg	ctc	tat	gta	aca	ctt	cct	cag	atg	agc	caa	ttt	aca	tgt	gaa	823	
139	Glu	Val	Leu	Tyr	Val	Thr	Leu	Pro	Gln	Met	Ser	Gln	Phe	Thr	Cys	Glu		
140	245					250				255			260					
142	gaa	gat	ttc	tac	ttt	cca	tgg	ctc	tta	att	att	atc	ttt	gga	ata	ttt	871	
143	Glu	Asp	Phe	Tyr	Phe	Pro	Trp	Leu	Leu	Ile	Ile	Ile	Phe	Gly	Ile	Phe		
144						265				270			275					
146	ggg	cta	aca	gtg	atg	cta	ttt	gta	ttc	tta	ttt	tct	aaa	cag	caa	agg	919	
147	Gly	Leu	Thr	Val	Met	Leu	Phe	Val	Phe	Leu	Phe	Ser	Lys	Gln	Gln	Arg		
148						280				285			290					
150	att	aaa	atg	ctg	att	ctg	ccc	cca	gtt	cca	aag	att	aaa	gga		967		
151	Ile	Lys	Met	Leu	Ile	Leu	Pro	Pro	Val	Pro	Val	Pro	Lys	Ile	Lys	Gly		
152						295				300			305					
154	atc	gat	cca	gat	ctc	ctc	aag	gaa	aaa	tta	gag	gag	gtg	aac	aca		1015	
155	Ile	Asp	Pro	Asp	Leu	Leu	Lys	Glu	Gly	Lys	Leu	Glu	Glu	Val	Asn	Thr		
156						310				315			320					
158	atc	tta	gcc	att	cat	gat	agc	tat	aaa	ccc	gaa	ttc	cac	agt	gat	gac		1063
159	Ile	Leu	Ala	Ile	His	Asp	Ser	Tyr	Lys	Pro	Glu	Phe	His	Ser	Asp	Asp		
160	325					330				335			340					
162	tct	tgg	gtt	gaa	ttt	att	gag	cta	gat	att	gat	gag	cca	gat	gaa	aag	1111	
163	Ser	Trp	Val	Glu	Ile	Glu	Leu	Asp	Ile	Asp	Glu	Pro	Asp	Glu	Lys			
164						345				350			355					
166	act	gag	gaa	tca	gac	aca	gac	ctt	cta	agc	agt	gac	cat	gag	aaa		1159	
167	Thr	Glu	Glu	Ser	Asp	Thr	Asp	Arg	Leu	Leu	Ser	Ser	Asp	His	Glu	Lys		
168						360				365			370					
170	tca	cat	agt	aac	cta	ggg	gtg	aag	gat	ggc	gac	tct	gga	cgt	acc	agc	1207	
171	Ser	His	Ser	Asn	Leu	Gly	Val	Lys	Asp	Gly	Asp	Ser	Gly	Arg	Thr	Ser		
172						375				380			385					
174	tgt	tgt	gaa	cct	gac	att	ctg	gag	act	gat	ttc	aat	gcc	aat	gac	ata		1255
175	Cys	Cys	Glu	Pro	Asp	Ile	Leu	Glu	Thr	Asp	Phe	Asn	Ala	Asn	Asp	Ile		
176						390				395			400					
178	cat	gag	ggt	acc	tca	gag	gtt	gct	cag	cca	cag	agg	tta	aaa	ggg	qaa		1303
179	His	Glu	Gly	Thr	Ser	Glu	Val	Ala	Gln	Pro	Gln	Arg	Leu	Lys	Gly	Glu		
180	405					410				415			420					
182	gca	gat	ctc	tta	tgc	ctt	gac	cag	aag	aat	caa	aat	aac	tca	cct	tat		1351
183	Ala	Asp	Leu	Leu	Cys	Leu	Asp	Gln	Lys	Asn	Gln	Asn	Asn	Ser	Pro	Tyr		
184						425				430			435					
186	cat	gat	gct	tgc	cct	gct	act	cag	cag	ccc	agt	gtt	atc	caa	gca	gag		1399
187	His	Asp	Ala	Cys	Pro	Ala	Thr	Gln	Gln	Pro	Ser	Val	Ile	Gln	Ala	Glu		
188						440				445			450					
190	aaa	aac	aaa	cca	caa	cca	ctt	cct	act	gaa	gga	gct	gag	tca	act	cac		1447
191	Lys	Asn	Lys	Pro	Gln	Pro	Leu	Pro	Thr	Glu	Gly	Ala	Glu	Ser	Thr	His		
192						455				460			465					
194	caa	gct	gcc	cat	att	cag	cta	agc	aat	cca	agt	tca	ctg	tca	aac	atc		1495
195	Gln	Ala	Ala	His	Ile	Gln	Leu	Ser	Asn	Pro	Ser	Ser	Leu	Ser	Asn	Ile		
196						470				475			480					
198	gac	ttt	tat	gcc	cag	gtg	agc	gac	att	aca	cca	gca	ggt	agt	gtg	gtc		1543
199	Asp	Phe	Tyr	Ala	Gln	Val	Ser	Asp	Ile	Thr	Pro	Ala	Gly	Ser	Val	Val		

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200	485	490	495	500	
202	cct tcc ccg ggc caa aag aat aag gca ggg atg tcc caa tgt gac atg				1591
203	Leu Ser Pro Gly Gln Lys Asn Lys Ala Gly Met Ser Gln Cys Asp Met				
204	505	510	515		
206	cac ccg gaa atg gtc tca ctc tgc caa gaa aac ttc ctt atg gac aat				1639
207	His Pro Glu Met Val Ser Leu Cys Gln Glu Asn Phe Leu Met Asp Asn				
208	520	525	530		
210	gcc tac ttc tgt gag gca gat gcc aaa aag tgc atc cct gtg gct cct				1687
211	Ala Tyr Phe Cys Glu Ala Asp Ala Lys Lys Cys Ile Pro Val Ala Pro				
212	535	540	545		
214	cac atc aag gtt gaa tca cac ata cag cca agc tta aac caa gag gac				1735
215	His Ile Lys Val Glu Ser His Ile Gln Pro Ser Leu Asn Gln Glu Asp				
216	550	555	560		
218	att tac atc acc aca gaa agc ctt acc act gct gct ggg agg cct ggg				1783
219	Ile Tyr Ile Thr Thr Glu Ser Leu Thr Thr Ala Ala Gly Arg Pro Gly				
220	565	570	575	580	
222	aca gga gaa cat gtt cca ggt tct gag atg cct gtc cca gac tat acc				1831
223	Thr Gly Glu His Val Pro Gly Ser Glu Met Pro Val Pro Asp Tyr Thr				
224	585	590	595		
226	tcc att cat ata gta cag tcc cca cag ggc ctc ata ctc aat gcg act				1879
227	Ser Ile His Ile Val Gln Ser Pro Gln Gly Leu Ile Leu Asn Ala Thr				
228	600	605	610		
230	gcc ttg ccc ttg cct gac aaa gag ttt ctc tca tca tgt ggc tat gtg				1927
231	Ala Leu Pro Leu Pro Asp Lys Glu Phe Leu Ser Ser Cys Gly Tyr Val				
232	615	620	625		
234	agc aca gac caa ctg aac aaa atc atg cct tag cctttcttg gtttccaaag				1980
235	Ser Thr Asp Gln Leu Asn Lys Ile Met Pro				
236	630	635			
238	agctacgtat ttaatagcaa agaattgact gggcaataa cgtttaagcc aaaacaatgt				2040
240	ttaaacctt tttggggag tgacaggatg gggatggat tctaaaatgc cttttcccaa				2100
242	aatgttgaaa tatgatgtta aaaaaataaag aagaatgctt aatcagatag atattcctat				2160
244	tgtgcaatgt aaatatttta aagaattgtg tcagactgtt tagtagcagt gattgtctta				2220
246	atattgtggg tgttaatttt tgatactaag cattgaatgg ctatgtttt aatgtatagt				2280
248	aaatcacgct tttgaaaaaa gcgaaaaaat caggtggctt ttgcgggtca ggaaaattga				2340
250	atgcaaaacca tagcacaggc taatttttt ttgtttctta aataagaaac ttttttattt				2400
252	aaaaaaactaa aaactagagg tgagaaaattt aaactataag caagaaggca aaaatagtt				2460
254	gatatatgtaa aacatttact ttgacataaa gttgataaag attttttaat aatttagact				2520
256	tcaagcatgg ctatttata ttacactaca cactgtgtac tgcagttgtt atgaccctc				2580
258	taaggagtgt agcaactaca gtctaaagct gtttaatgt tttggccaaat gcacctaag				2640
260	aaaaacaaac tcgttttta caaagccctt ttataccctc ccagactct tcaacaattc				2700
262	taaaatgatt gtatgtatct gcattattgg aatataattt ttttatctga atttttaaac				2760
264	aagtatttgt taatttagaa aactttaaag cgtttgcaca gatcaactt ccaggcacca				2820
266	aaagaagtaa aagcaaaaaa gaaaaccttt cttcacaaa tcttgggtga tgccaaaaaa				2880
268	aaatacatgc taagagaagt agaaatcata gctggtcac actgaccaag atacttaagt				2940
270	gctgcaatttgcacgcggagt gagtttttta gtgcgtgcag atggtagagataagatcta				3000
272	tagcctctgc agcggaatct gttcacaccc aacttgggtt tgctacataa ttatccagga				3060
274	agggagataag gtacaagaag cattttgtaa gttgaagcaa atcgaatgaa attaactggg				3120
276	taatgaaaca aagaggtaa gaaataagg tttgtttcac agcctataac cagacacata				3180
278	ctcatttttc atgataatga acagaacata gacagaagaa acaaggttt cagtccccac				3240

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; N Pos. 2636,2666,2759,2789,3326,3352,3503,3666,3668
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Seq#:100; N Pos. 5528,5529,5530,5531,5532,5533,5534,5535,5536,5537,5538
Seq#:100; N Pos. 5539,5540,5541,5542,5543,5544,5545,5546,5547,5548,5549
Seq#:100; N Pos. 5550,5551,5552,5553,5554,5555,5556,5557,5558,5559,5560
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Seq#:100; N Pos. 5583,5584,5585,5586,5587,5588,5589,5590,5591,5592,5593
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VERIFICATION SUMMARY

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L:654 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:2632
M:341 Repeated in SeqNo=11
L:3137 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:98 after pos.:2400
M:341 Repeated in SeqNo=98
L:3336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:99 after pos.:2460
M:341 Repeated in SeqNo=99
L:3426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:100 after pos.:0
M:341 Repeated in SeqNo=100